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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372C

DATE: 06/28/2002

TIME: 14:12:02

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Output Set: N:\CRF3\06282002\J017372C.raw

3 <110> APPLICANT: Wolfrain, Lawrence A
4 Letterio, John J
6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
8 <130> FILE REFERENCE: 4239-61302
10 <140> CURRENT APPLICATION NUMBER: US 10/017,372C
11 <141> CURRENT FILING DATE: 2001-10-19
13 <150> PRIOR APPLICATION NUMBER: US 60/242,292
14 <151> PRIOR FILING DATE: 2000-10-20
16 <160> NUMBER OF SEQ ID NOS: 39
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 28
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Primer
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33 <211> LENGTH: 42
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35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Primer
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45 <211> LENGTH: 48
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47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: Primer
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56 <210> SEQ ID NO: 4
57 <211> LENGTH: 45
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Primer
64 <400> SEQUENCE: 4
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68 <210> SEQ ID NO: 5

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69 <211> LENGTH: 45
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74 <223> OTHER INFORMATION: Primer
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82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer
88 <400> SEQUENCE: 6
89 cttgtcgtcg tcattcttgt agtctcggcg gtgccgggag ctgtg 45
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 8
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Synthetic oligopeptide
100 <400> SEQUENCE: 7
102 Asp Tyr Lys Asp Asp Asp Lys
103 1 5
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 1197
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Fusion oligonucleotide
114 <220> FEATURE:
115 <221> NAME/KEY: CDS
116 <222> LOCATION: (1)..(1197)
117 <223> OTHER INFORMATION:
120 <220> FEATURE:
121 <221> NAME/KEY: misc_feature
122 <222> LOCATION: (278)..(279)
123 <223> OTHER INFORMATION: Maturation cleavage site
126 <400> SEQUENCE: 8
127 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
128 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
129 1 5 10 15
131 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
132 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
133 20 25 30
135 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
136 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
137 35 40 45
139 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192

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140	Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser	
141		50					55					60					
143	cag	ggg	gac	gtg	ccg	ccc	ggc	ccg	ctg	cct	gag	gca	gta	ctg	gct	ctt	240
144	Gln	Gly	Asp	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu	
145	65					70				75					80		
147	tac	aac	agt	acc	cgc	gac	cgg	gta	gcc	ggg	gaa	agt	gtc	gaa	ccg	gag	288
148	Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Val	Glu	Pro	Glu	
149					85					90					95		
151	ccc	gag	cca	gag	gcg	gac	tac	tac	gcc	aag	gag	gtc	acc	cgc	gtg	cta	336
152	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu	
153				100					105					110			
155	atg	gtg	gaa	agc	ggc	aac	caa	atc	tat	gat	aaa	ttc	aag	ggc	acc	ccc	384
156	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys	Gly	Thr	Pro	
157			115				120					125					
159	cac	agc	tta	tat	atg	ctg	ttc	aac	acg	tcg	gag	ctc	cgg	gaa	gcg	gtg	432
160	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg	Glu	Ala	Val	
161		130				135					140						
163	ccg	gaa	cct	gta	ttg	ctc	tct	cgg	gca	gag	ctg	cgc	ctg	ctg	agg	ctc	480
164	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Leu	Arg	Leu	
165	145				150					155					160		
167	aag	tta	aaa	gtg	gag	cag	cac	gtg	gag	cta	tac	cag	aaa	tac	agc	aat	528
168	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	
169				165					170					175			
171	gat	tcc	tgg	cgc	tac	ctc	agc	aac	cgg	ctg	ctg	gcc	ccc	agt	gac	tca	576
172	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	Ser	Asp	Ser	
173				180				185					190				
175	ccg	gag	tgg	ctg	tcc	ttt	gat	gtc	acc	gga	gtt	gtg	cgg	cag	tgg	ctg	624
176	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	
177		195					200					205					
179	acc	cgc	aga	gag	gct	ata	gag	ggt	ttt	cgc	ctc	agt	gcc	cac	tct	tcc	672
180	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Ser	Ser	
181		210				215						220					
183	tct	gac	agc	aaa	gat	aac	aca	ctc	cac	gtg	gaa	att	aac	ggg	ttc	aat	720
184	Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn	
185	225				230					235					240		
187	tct	ggc	cgc	cgg	ggt	gac	ctg	gcc	acc	att	cac	ggc	atg	aac	cgg	ccc	768
188	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro	
189				245				250						255			
191	ttc	ctg	ctc	ctc	atg	gcc	acc	ccg	ctg	gag	agg	gcc	cag	cac	ctg	cac	816
192	Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His	
193			260					265					270				
195	agc	tcc	cgg	cac	cgc	cga	gac	tac	aag	gat	gac	gac	gac	aag	gcc	ctg	864
196	Ser	Ser	Arg	His	Arg	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu	
197			275				280						285				
199	gat	acc	aac	tac	tgc	ttc	agc	tcc	acg	gag	aag	aac	tgc	tgc	gtg	cgg	912
200	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	
201		290				295						300					
203	cag	ctc	tac	att	gac	ttc	cgg	aag	gac	ctg	ggc	tgg	aag	tgg	att	cat	960
204	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	

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205 305          310          315          320
207 gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac      1008
208 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
209          325          330          335
211 atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac      1056
212 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
213          340          345          350
215 cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg      1104
216 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
217          355          360          365
219 ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg      1152
220 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
221          370          375          380
223 gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga      1197
224 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
225 385          390          395
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229 <211> LENGTH: 398
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Fusion oligonucleotide
236 <220> FEATURE:
237 <221> NAME/KEY: misc_feature
238 <222> LOCATION: (278)..(279)
239 <223> OTHER INFORMATION: Maturation cleavage site
241 <400> SEQUENCE: 9
243 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
244 1          5          10          15
247 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
248          20          25          30
251 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
252          35          40          45
255 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
256          50          55          60
259 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
260 65          70          75          80
263 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
264          85          90          95
267 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
268          100          105          110
271 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
272          115          120          125
275 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
276          130          135          140
279 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
280 145          150          155          160
283 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
284          165          170          175

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287 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
288          180          185          190
291 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
292          195          200          205
295 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
296          210          215          220
299 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
300 225          230          235          240
303 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
304          245          250          255
307 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
308          260          265          270
311 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
312          275          280          285
315 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
316          290          295          300
319 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
320 305          310          315          320
323 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
324          325          330          335
327 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
328          340          345          350
331 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
332          355          360          365
335 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
336          370          375          380
339 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
340 385          390          395

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343 <210> SEQ ID NO: 10

344 <211> LENGTH: 362

345 <212> TYPE: DNA

346 <213> ORGANISM: Artificial Sequence

348 <220> FEATURE:

349 <223> OTHER INFORMATION: Fusion oligonucleotide

351 <400> SEQUENCE: 10

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356 attcatgaac ccaagggctc catgccatt tctgcctggg gccctgtccc tacatctgga      180
358 gcttagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt      240
360 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gccatcgtg tactacgtgg      300
362 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttctgc aagtgcagct      360
364 ga

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368 <211> LENGTH: 120

369 <212> TYPE: PRT

370 <213> ORGANISM: Artificial Sequence

372 <220> FEATURE:

373 <223> OTHER INFORMATION: Fusion oligopeptide

375 <220> FEATURE:

VERIFICATION SUMMARY

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